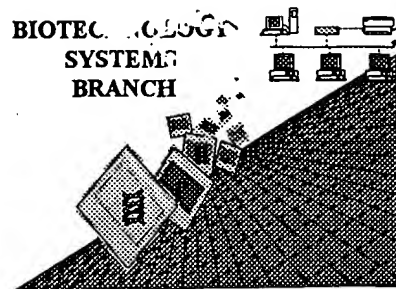


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/509,196

Source: 1643

Date Processed by STIC: 7/12/2000

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

JUL 28 2000

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER: TECH CENTER 1600/2800

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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do not use under new sequence rules
~~SEQUENCE LISTING~~

Does Not Comply
Corrected Diskette Needed

<110> ~~Applicant:~~ Garvan Institute of Medical Research
<120> ~~Title of Invention:~~ A potential effector for the Grb7 family of signalling proteins.
<140> ~~Current Application Number:~~ US 09/509,196
<141> ~~Current Filing Date:~~ 2000-03-23
<150> ~~Prior Application Number:~~ P09388
<151> ~~Prior Application Filing Date:~~ 1997-09-23
<160> ~~Number of ID SEQ Nos:~~ 2
<170> ~~Software:~~ PatentIn Ver. 2.0
<210> ~~SEQ ID NO:~~ 1
<211> ~~length:~~ 3400
<212> ~~Type:~~ DNA
<213> ~~Organism:~~ Homo sapiens

Please consult
sample sequence
listing, attached
is back, for valid
format.

<400> ~~Sequence:~~ 1
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catggtgcag accccaatgc tcgagataat tggaattata ctctctcca tgaagctgca 120
attaaaggaa agattgatgt ttgcattgtg ctgttacagc atggagctga gccaccatc 180
cgaaatacag atggaaggac agcattggat ttagcagatc catctgccaa agcagtgtt 240
actggtgaat ataagaaaga tgaactctta gaaagtgcga ggagtggcaa tgaagaaaaa 300
atgatggctc tactcacacc attaatgtc aactgccacg caagtgatgg cagaaagtca 360
actccattac atttggcagc aggatataac agagtaaaga ttgtacagct gttactgcaa 420
catggacgtg atgtccatgc taaagataaa ggtgatctgg taccattaca caatgcctgt 480
tcttatggtc attatgaagt aactgaactt ttggtcaagc atggtggctg tgtaaattgca 540
atggacttgt ggcaattcac tcctcttcac gaggcagctt ctaagaacag ggttgaagta 600
tgttctcttc tcttaagtta tgggtgcagc ccaacactgc tcaattgtaa gaataaaagt 660
gctatagact tggctccac accacagtta aaagaaagat tagcatatga atttaaaggc 720
cactcgttgc tgcaagctgc acgagaagct gatgttactc gaatcaaaaa acatctctct 780
ctggaaatgg tgaatttcaa gcatcctcaa acacatgaaa cagcattgca ttgtgctgct 840
gcatctccat atcccaaaag aaagcaaata tgtgaactgt tgctaagaaa aggagcaaac 900
atcaatgaaa agactaaaga attcttgact cctctgcacg tggcatctga gaaagctcat 960
aatgatgttg ttgaagtagt ggtgaaacat gaagcaaagg ttaatgctct ggataatctt 1020
ggtcagactt ctctacacag agctgcatat tgtggtcatc tacaacctg ccgcctactc 1080
ctgagctatg ggtgtgatcc taacattata tcccttcagg gctttactgc ttacagatg 1140
ggaaatgaaa atgtacagca actcctccaa gagggatatc cattaggtaa ttcagaggca 1200
gacagacaat tgctggaagc tgcaaaggct ggagatgtcg aaactgtaaa aaaactgtgt 1260
actgttcaga gtgtcaactg cagagacatt gaagggcgct agtctacacc acttcatttt 1320
gcagctgggt ataacagagt gtccgtggtg gaatatctgc tacagcatgg agctgatgtg 1380
catgctaaag ataaaggagg ccttgtacct ttgcacaatg catgttctta cggacattat 1440
gaagttgcag aacttcttgt taaacatgga gcagtagtta atgtagctga tttatggaaa 1500
tttacacctt tacatgaagc agcagcaaaa ggaaaatatg aaatttgcaa acttctgctc 1560
cagcatggtg cagaccctac aaaaaaaaac agggatggaa atactccttt ggatcttgtt 1620
aaagatggag atacagatat tcaagatctg cttaggggag atgcagcttt gctagatgct 1680
gccaagaagg gttgttttag cagagtgaag aagttgtctt ctctgataa tgtaaattgc 1740
cgcgataccc aaggcagaca ttcaacacct ttacatttag cagctgggta taataattta 1800
gaagttgcag agtatttgtt acaacacgga gctgatgtga atgccaaga caaaggagga 1860
cttattcctt tacataatgc agcatcttac gggcatgtag atgtagcagc tctactaata 1920

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Please review the
Sequenc Listing to ensure that a corres ponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

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```

aagtataatg catctctcaa tgccacggac aaatgggctt tcacaccttt gcacgaagca 1980
gccccaaagg gacgaacaca gctttgtgct ttgttgctag cccatggagc tgacccgact 2040
cttaaaaatc aggaaggaca aacaccttta gatttagttt cagcagatga tgtcagcgct 2100
cttctgacag cagccatgcc cccatctgct ctgccctctt gttacaagcc tcaagtgtct 2160
aatggtgtga gaagcccagg agccactgca gatgctctct cttcaggtcc atctagccca 2220
tcaagccttt ctgcagccag cagtcttgac aacttatctg ggagtttttc agaactgtct 2280
tcagtagtta gttcaagtgg aacagagggg gcttccagtt tggagaaaaa ggaggttcca 2340
ggagtagatt ttagcataac tcaattcgta aggaatcttg gacttgagca cctaattggat 2400
atatttgaga gagaacagat cactttggat gtattagttg agatggggca caaggagctg 2460
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acaattctta tagatctgtc tcctgatgat aaagagtttc agtctgtgga ggaagagatg 2640
caaagtacag ttcgagagca cagagatgga ggtcatgcag gtggaatctt caacagatac 2700
aatattctca agattcagaa ggtttgtaac aagaaactat gggaaagata cactcaccgg 2760
agaaaagaag tttctgaaga aaaccacaac catgccaatg aacgaatgct atttcatggg 2820
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ggtagtggg gagctggcat ttattttgct gaaaactctt ccaaaagcaa tcaatatgta 2940
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cacaggcagc tgctcttttg ccgggtaacc ttgggaaagt ctttcttgca gttcagtgc 3060
atgaaaatgg cacattctcc tccagggtcat cactcagtca ctggtaggcc cagtgtaaat 3120
ggcctagcat tagctgaata tgttatttac agaggagAAC aggcctatcc tgagtattta 3180
attacttacc agattatgag gcctgaagggt atggctgatg gataaatagt tattttaaga 3240
aactaattcc actgaaccta aaatcatcaa agcagcagtg gcctctacgt ttactcctt 3300
tgctgaaaaa aaatcatctt gcccacaggc ctgtggcaaa aggataaaaa tgtgaacgaa 3360
gtttaacatt ctgacttgat aaagctttta taatgtacag 3400

```

(2137) ~~SEQ ID NO:~~ 2(2117) ~~Length:~~ 1074(2127) ~~Type:~~ PRT(2137) ~~Organism:~~ Homo sapiens(4007) ~~Sequence:~~ 2

```

Ile Pro Leu His Asn Ala Cys Ser Phe Gly His Ala Glu Val Val Asn
1           5           10           15

```

```

Leu Leu Leu Arg His Gly Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn
20           25           30

```

```

Tyr Thr Pro Leu His Glu Ala Ala Ile Lys Gly Lys Ile Asp Val Cys
35           40           45

```

```

Ile Val Leu Leu Gln His Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp
50           55           60

```

```

Gly Arg Thr Ala Leu Asp Leu Ala Asp Pro Ser Ala Lys Ala Val Leu
65           70           75           80

```

```

Thr Gly Glu Tyr Lys Lys Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly
85           90           95

```

```

Asn Glu Glu Lys Met Met Ala Leu Leu Thr Pro Leu Asn Val Asn Cys
100          105          110

```

```

His Ala Ser Asp Gly Arg Lys Ser Thr Pro Leu His Leu Ala Ala Gly
115          120          125

```

```

Tyr Asn Arg Val Lys Ile Val Gln Leu Leu Leu Gln His Gly Arg Asp

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130

135

140

Val His Ala Lys Asp Lys Gly Asp Leu Val Pro Leu His Asn Ala Cys
145 150 155 160

Ser Tyr Gly His Tyr Glu Val Thr Glu Leu Leu Val Lys His Gly Gly
165 170 175

Cys Val Asn Ala Met Asp Leu Trp Gln Phe Thr Pro Leu His Glu Ala
180 185 190

Ala Ser Lys Asn Arg Val Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly
195 200 205

Ala Asp Pro Thr Leu Leu Asn Cys Lys Asn Lys Ser Ala Ile Asp Leu
210 215 220

Ala Pro Thr Pro Gln Leu Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly
225 230 235 240

His Ser Leu Leu Gln Ala Ala Arg Glu Ala Asp Val Thr Arg Ile Lys
245 250 255

Lys His Leu Ser Leu Glu Met Val Asn Phe Lys His Pro Gln Thr His
260 265 270

Glu Thr Ala Leu His Cys Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys
275 280 285

Gln Ile Cys Glu Leu Leu Leu Arg Lys Gly Ala Asn Ile Asn Glu Lys
290 295 300

Thr Lys Glu Phe Leu Thr Pro Leu His Val Ala Ser Glu Lys Ala His
305 310 315 320

Asn Asp Val Val Glu Val Val Val Lys His Glu Ala Lys Val Asn Ala
325 330 335

Leu Asp Asn Leu Gly Gln Thr Ser Leu His Arg Ala Ala Tyr Cys Gly
340 345 350

His Leu Gln Thr Cys Arg Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn
355 360 365

Ile Ile Ser Leu Gln Gly Phe Thr Ala Leu Gln Met Gly Asn Glu Asn
370 375 380

Val Gln Gln Leu Leu Gln Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala
385 390 395 400

Asp Arg Gln Leu Leu Glu Ala Ala Lys Ala Gly Asp Val Glu Thr Val
405 410 415

Lys Lys Leu Cys Thr Val Gln Ser Val Asn Cys Arg Asp Ile Glu Gly
420 425 430

Arg Gln Ser Thr Pro Leu His Phe Ala Ala Gly Tyr Asn Arg Val Ser

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435

440

445

Val Val Glu Tyr Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp
 450 455 460

Lys Gly Gly Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr
 465 470 475 480

Glu Val Ala Glu Leu Leu Val Lys His Gly Ala Val Val Asn Val Ala
 485 490 495

Asp Leu Trp Lys Phe Thr Pro Leu His Glu Ala Ala Ala Lys Gly Lys
 500 505 510

Tyr Glu Ile Cys Lys Leu Leu Leu Gln His Gly Ala Asp Pro Thr Lys
 515 520 525

Lys Asn Arg Asp Gly Asn Thr Pro Leu Asp Leu Val Lys Asp Gly Asp
 530 535 540

Thr Asp Ile Gln Asp Leu Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala
 545 550 555 560

Ala Lys Lys Gly Cys Leu Ala Arg Val Lys Lys Leu Ser Ser Pro Asp
 565 570 575

Asn Val Asn Cys Arg Asp Thr Gln Gly Arg His Ser Thr Pro Leu His
 580 585 590

Leu Ala Ala Gly Tyr Asn Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln
 595 600 605

His Gly Ala Asp Val Asn Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu
 610 615 620

His Asn Ala Ala Ser Tyr Gly His Val Asp Val Ala Ala Leu Leu Ile
 625 630 635 640

Lys Tyr Asn Ala Ser Leu Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro
 645 650 655

Leu His Glu Ala Ala Gln Lys Gly Arg Thr Gln Leu Cys Ala Leu Leu
 660 665 670

Leu Ala His Gly Ala Asp Pro Thr Leu Lys Asn Gln Glu Gly Gln Thr
 675 680 685

Pro Leu Asp Leu Val Ser Ala Asp Asp Val Ser Ala Leu Leu Thr Ala
 690 695 700

Ala Met Pro Pro Ser Ala Leu Pro Ser Cys Tyr Lys Pro Gln Val Leu
 705 710 715 720

Asn Gly Val Arg Ser Pro Gly Ala Thr Ala Asp Ala Leu Ser Ser Gly
 725 730 735

Pro Ser Ser Pro Ser Ser Leu Ser Ala Ala Ser Ser Leu Asp Asn Leu

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740	745	750
Ser Gly Ser Phe Ser Glu Leu Ser Ser Val Val Ser Ser Ser Gly Thr		
755	760	765
Glu Gly Ala Ser Ser Leu Glu Lys Lys Glu Val Pro Gly Val Asp Phe		
770	775	780
Ser Ile Thr Gln Phe Val Arg Asn Leu Gly Leu Glu His Leu Met Asp		
785	790	795
Ile Phe Glu Arg Glu Gln Ile Thr Leu Asp Val Leu Val Glu Met Gly		
805	810	815
His Lys Glu Leu Lys Glu Ile Gly Ile Asn Ala Tyr Gly His Arg His		
820	825	830
Lys Leu Ile Lys Gly Val Glu Arg Leu Ile Ser Gly Gln Gln Gly Leu		
835	840	845
Asn Pro Tyr Leu Thr Leu Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile		
850	855	860
Asp Leu Ser Pro Asp Asp Lys Glu Phe Gln Ser Val Glu Glu Glu Met		
865	870	875
Gln Ser Thr Val Arg Glu His Arg Asp Gly Gly His Ala Gly Gly Ile		
885	890	895
Phe Asn Arg Tyr Asn Ile Leu Lys Ile Gln Lys Val Cys Asn Lys Lys		
900	905	910
Leu Trp Glu Arg Tyr Thr His Arg Arg Lys Glu Val Ser Glu Glu Asn		
915	920	925
His Asn His Ala Asn Glu Arg Met Leu Phe His Gly Ser Pro Phe Val		
930	935	940
Asn Ala Ile Ile His Lys Gly Phe Asp Glu Arg His Ala Tyr Ile Gly		
945	950	955
Gly Met Phe Gly Ala Gly Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser		
965	970	975
Asn Gln Tyr Val Tyr Gly Ile Gly Gly Gly Thr Gly Cys Pro Val His		
980	985	990
Lys Asp Arg Ser Cys Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg		
995	1000	1005
Val Thr Leu Gly Lys Ser Phe Leu Gln Phe Ser Ala Met Lys Met Ala		
1010	1015	1020
His Ser Pro Pro Gly His His Ser Val Thr Gly Arg Pro Ser Val Asn		
1025	1030	1035
Gly Leu Ala Leu Ala Glu Tyr Val Ile Tyr Arg Gly Glu Gln Ala Tyr		

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1045

1050

1055

Pro Glu Tyr Leu Ile Thr Tyr Gln Ile Met Arg Pro Glu Gly Met Val
1060 1065 1070

Asp Gly

Appendix A To Subpart C to Part 1—Sample Sequence Listing

<110> Smith, John

Smith, Jane

<120> Example of a Sequence Listing

<130> 01-00001

<140> US 08/999,999

<141> 1998-02-28

<150> EP 91000000

<151> 1997-12-31

<160> 2

<170> PatentIn ver. 2.0

<210> 1

<211> 403

<212> DNA

<213> Paramecium aurelia

<220>

<221> CDS

<222> 341..394

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a

Protease from Paramecium sp.

<303> Journal of Fictional Genes

<304> 1

<305> 4

<306> 1 - 7

<307> 1988-06-20

<400> 1

ctactctact ctactctcat ctactatctt ctttggatct ctgagtctgc ctgagtggta 60

ctcttgagtc ctggagatct ctctctcac atgtgatcgt cgagactgac cgatagatcg 120

ctgactgact ctgagatagt cgagcccgta cgagaccgt cgagggtgac agagagtggg 180

cgcgtagcgcg cagagcgccg cgccggtgcg cgcgcgagtgc cgcggtgggc cgcgcgaggg 240

ctttcgcggc agcggcggcg ctttcggcg cgcgcccgtc cgccctaga cctgagaggt 300

ctctcttcc ctctcttca ctagagaggt ctatatatac atg gtt tca atg ttc 355

Met Val Ser Met Phe

agc ttg tct ttc aaa tgg cct gga ttt tgt ttg ttt gtt tgtttgctc

403

Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val

- 10

15

<210> 2

<211> 18

<212> PRT

<213> *Paramecium aurelia*

<400> 2

Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu

1

5

10

15

Phe Val

ed: May 22, 1998.

A. Lehman,

ant Secretary of Commerce and
Commissioner of Patents and Trademarks.

oc. 98-14194 Filed 5-29-98; 8:45 am]

CODE 3510-16-C

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names, and/or Initials.	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO: #:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

		in feature	base was used in a sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	0
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	0
<302>	Title		0
<303>	Journal		0
<304>	Volume		0
<305>	Issue		0
<306>	Pages		0
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	0
<308>	Database Accession Number	Accession number assigned by database including database name	0
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	0
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	0

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	O
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	M

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(c) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;